

295899US0PCT.ST25
SEQUENCE LISTING

<110> Kudo, Toshiaki
Motoyama, Takayuki

<120> METHOD OF SCREENING FUNGUS-SPECIFIC ANTIMICROBIAL AGENT AND KIT
THEREFOR

<130> 295899US0PCT

<140> US 10/591,464
<141> 2006-09-01

<150> PCT/JPO5/004272
<151> 2005-03-04

<150> JP 2004-061273
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<170> PatentIn version 3.3

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 Glu Gly Ile Leu Gly Gly Gln Ala Asp Val Glu Gly Val Gln Gly Met
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 Trp Asn Glu Leu Thr Val Asn Val Asn Ala Met Ala Asn Asn Leu Thr
 355 360 365

Thr Gln Val Arg Asp Ile Ile Lys Val Thr Thr Ala Val Ala Lys Gly
 370 375 380
 Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Arg Gly Glu Ile Phe Glu
 385 390 395
 Leu Lys Lys Thr Ile Asn Ser Met Val Asp Gln Leu Gln Gln Phe Ala
 405 410 415
 Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu Gly Arg Leu
 420 425 430
 Gly Gly Gln Ala Thr Val His Asp Val Gln Gly Thr Trp Arg Asp Leu
 435 440 445
 Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr Gln Val Arg
 450 455 460
 Glu Ile Ala Lys Val Thr Thr Ala Val Ala Lys Gly Asp Leu Thr Lys
 465 470 475 480
 Lys Ile Gly Val Glu Val Gln Gly Glu Ile Leu Asp Leu Lys Asn Thr
 485 490 495
 Ile Asn Thr Met Val Asp Arg Leu Gly Thr Phe Ala Phe Glu Val Ser
 500 505 510
 Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr Leu Gly Gly Gln Ala
 515 520 525
 Gln Val Asp Asn Val Glu Gly Lys Trp Lys Asp Leu Thr Glu Asn Val
 530 535 540
 Asn Thr Met Ala Ser Asn Leu Thr Ser Gln Val Arg Gly Ile Ser Thr
 545 550 555 560
 Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Arg Lys Ile Glu Val
 565 570 575
 Glu Ala Lys Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile Asn Asn Met
 580 585 590
 Val Asp Arg Leu Ser Ile Phe Cys Asn Glu Val Gln Arg Val Ala Lys
 595 600 605
 Asp Val Gly Val Asp Gly Ile Met Gly Gly Gln Ala Asp Val Ala Gly
 610 615 620
 Leu Lys Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn Thr Met Ala
 625 630 635 640

Asn Asn Leu Thr Ala Gln Val Arg Ala Phe Gly Asp Ile Thr Asn Ala
 645 650 655
 Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Glu Val Glu Ala Ser Gly
 660 665 670
 Glu Met Asp Glu Leu Lys Lys Lys Ile Asn Gln Met Val Tyr Asn Leu
 675 680 685
 Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg Glu Ala Ala Glu Leu
 690 695 700
 Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn Met Ser His Glu Ile
 705 710 715 720
 Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu Thr Leu Asp
 725 730 735
 Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile Val Asn Ser
 740 745 750
 Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu Asp Leu Ser
 755 760 765
 Lys Ile Glu Ala Arg Arg Met Val Ile Glu Glu Ile Pro Tyr Thr Leu
 770 775 780
 Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val Lys Glu Thr
 785 790 795 800
 Glu Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp His Ser Val Pro Asp
 805 810 815
 His Val Val Gly Asp Ser Phe Arg Leu Arg Gln Ile Ile Leu Asn Leu
 820 825 830
 Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val Ser Leu Thr
 835 840 845
 Ile Gln Lys Ala Ser Ser Val Gln Cys Ser Thr Glu Glu Tyr Ala Ile
 850 855 860
 Glu Phe Val Val Ser Asp Thr Gly Ile Gly Ile Pro Ala Asp Lys Leu
 865 870 875 880
 Asp Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser Met Thr Arg
 885 890 895
 Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Arg Leu Val
 900 905 910

Asn Leu Met Gly Gly Asp Val Trp Val Lys Ser Glu Tyr Gly Lys Gly
 915 920 925
 Ser Lys Phe Phe Phe Thr Cys Val Val Arg Leu Ala Asn Asp Asp Ile
 930 935 940
 Ser Leu Ile Ala Lys Gln Leu Asn Pro Tyr Lys Ser His Gln Val Leu
 945 950 955 960
 Phe Ile Asp Lys Gly Arg Thr Gly His Gly Pro Glu Ile Ala Lys Met
 965 970 975
 Leu His Gly Leu Gly Leu Val Pro Ile Val Val Asp Ser Glu Arg Asn
 980 985 990
 Pro Ala Leu Glu Lys Ala Arg Ala Ala Gly Gln Ala Pro Tyr Asp Val
 995 1000 1005
 Ile Ile Val Asp Ser Ile Glu Asp Ala Arg Arg Leu Arg Ser Val
 1010 1015 1020
 Asp Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu Ala Pro Val Val
 1025 1030 1035
 His Val Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile Thr Ser Tyr
 1040 1045 1050
 Met Thr Thr Pro Cys Gln Leu Ile Asp Leu Gly Asn Gly Met Val
 1055 1060 1065
 Pro Ala Leu Glu Asn Arg Ala Thr Pro Ser Leu Ala Asp Asn Thr
 1070 1075 1080
 Lys Ser Phe Glu Ile Leu Leu Ala Glu Asp Asn Thr Val Asn Gln
 1085 1090 1095
 Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr
 1100 1105 1110
 Val Val Gly Asn Gly Glu Glu Ala Val Glu Ala Val Lys Arg Lys
 1115 1120 1125
 Lys Phe Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly
 1130 1135 1140
 Gly Phe Glu Ala Thr Ala Lys Ile Arg Glu Tyr Glu Arg Ser Leu
 1145 1150 1155
 Gly Ser Gln Arg Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met
 1160 1165 1170

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Met Gly Asp Arg Glu Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr
 1175 1180 1185
 Leu Ser Lys Pro Leu Gln Gln Asn His Leu Ile Gln Thr Ile Leu
 1190 1195 1200
 Lys Cys Ala Thr Leu Gly Gly Gln Leu Leu Glu Lys Asn Arg Glu
 1205 1210 1215
 Arg Glu Leu Thr Arg Ala Ala Asp Ala Val Thr Gly Gly Arg Arg
 1220 1225 1230
 Asp Asn Gly Met Tyr Ser Ala Ser Gln Ala Ala Gln His Ala Ala
 1235 1240 1245
 Leu Arg Pro Pro Leu Ala Thr Arg Gly Leu Thr Ala Ala Asp Ser
 1250 1255 1260
 Leu Val Ser Gly Leu Glu Ser Pro Ser Ile Val Thr Ala Asp Lys
 1265 1270 1275
 Glu Asp Pro Leu Ser Arg Ala Arg Ala Ser Leu Ser Glu Pro Asn
 1280 1285 1290
 Ile His Lys Ala Ser
 1295